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Clustalw Your results

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CLUSTAL W (1.82) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: FixL      505 aa
Sequence 2: SEQ76     153 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 17
Guide tree      file created: [/ebi/extserv/old-work/clust
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:           Delayed
Sequence:2      Score:1222
Alignment Score 83
CLUSTAL-Alignment file created [/ebi/extserv/old-work/clustal]

```

clustalw-20030805-21191830.aln

CLUSTAL W (1.82) multiple sequence alignment

FixL	MAPTRVTHPPDDGRGEHFRVRIEGFGVGTWDLKTLKWTALDWSDTAI
SEQ76	-----VLSEGEWQLVLHVWAKVEADVA- :.. * *;* *;*.* :*.*
FixL	LFLSRLEPDDRERVESAIKRVSERGGGFDVSVFVAGTSNAGQWIR/

clustalw-20030805-21191830.dnd

(FixL:0.41176,SEQ76:0.41176);

Please contact support@ebi.ac.uk with any problems or suggestions regarding this site.



PubMed	Nucleotide	Protein	Genome	Structure	PMC	Taxonomy	OMIM	Book
Search Protein <input type="text"/> for <input type="button" value="Go"/> <input type="button" value="Clear"/>								
Display <input type="button" value="default"/>		Limits <input type="button" value=""/>	Preview/Index <input type="button" value=""/>		History <input type="button" value=""/>	Clipboard <input type="button" value=""/>	Details <input type="button" value=""/>	
		Show: <input type="text" value="20"/> <input type="button" value=""/>	<input type="button" value="Send to"/> <input type="button" value=""/>		File <input type="button" value=""/>	<input type="button" value="Get Subsequence"/>		

1: P23222. Sensor protein fi...[gi:120207]

[BLink](#), [Domains](#), [Links](#)

LOCUS P23222 505 aa **linear** BCT 15-SEP-2003
DEFINITION Sensor protein fixL.
ACCESSION P23222
VERSION P23222 GI:120207
DBSOURCE swissprot: locus FIXL_BRAJA, accession P23222;
 class: standard.
 created: Nov 1, 1991.
 sequence updated: Nov 1, 1991.
 annotation updated: Sep 15, 2003.
 xrefs: gi: [39522](#), gi: [39523](#), gi: [3021308](#), gi: [3021311](#), gi: [27350985](#), gi: [27351017](#), gi: [7465577](#), pdb accession 1DRM, pdb accession 1LT0, pdb accession 1DP6, pdb accession 1DP8, pdb accession 1DP9, pdb accession 1LSV, pdb accession 1LSW, pdb accession 1LSX
 xrefs (non-sequence databases): InterProIPR003594, InterProIPR004358, InterProIPR003661, InterProIPR005467, InterProIPR001610, InterProIPR000700, InterProIPR000014, PfamPF02518, PfamPF00512, PfamPF00785, PfamPF00989, PRINTSPR00344, SMARTSM00387, SMARTSM00388, SMARTSM00086, SMARTSM00091, TIGRFAMsTIGR00229, PROSITEPS50109, PROSITEPS50113, PROSITEPS50112
KEYWORDS Sensory transduction; Transferase; Kinase; Phosphorylation; Heme; Transmembrane; Inner membrane; Nitrogen fixation; Repeat; Iron transport; 3D-structure; Complete proteome.
SOURCE Bradyrhizobium japonicum
ORGANISM Bradyrhizobium japonicum
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales; Bradyrhizobiaceae; Bradyrhizobium.
REFERENCE 1 (residues 1 to 505)
AUTHORS Anthamatten,D. and Hennecke,H.
TITLE The regulatory status of the fixL- and fixJ-like genes in Bradyrhizobium japonicum may be different from that in Rhizobium meliloti
JOURNAL Mol. Gen. Genet. 225 (1), 38-48 (1991)
MEDLINE [91155933](#)
PUBMED [2000090](#)
REMARK SEQUENCE FROM N.A.
 STRAIN=USDA 110spc4
REFERENCE 2 (residues 1 to 505)
AUTHORS Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiimi,T., Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K., Kohara,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M. and Tabata,S.
TITLE Complete genomic sequence of nitrogen-fixing symbiotic bacterium Bradyrhizobium japonicum USDA110
JOURNAL DNA Res. 9 (6), 189-197 (2002)
MEDLINE [22484998](#)
PUBMED [12597275](#)

REMARK SEQUENCE FROM N.A.
 STRAIN=USDA 110
 REFERENCE 3 (residues 1 to 505)
 AUTHORS Gong,W., Hao,B., Mansy,S.S., Gonzalez,G., Gilles-Gonzalez,M.A. and
 Chan,M.K.
 TITLE Structure of a biological oxygen sensor: a new mechanism for
 heme-driven signal transduction
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (26), 15177-15182 (1998)
 MEDLINE 99079986
 PUBMED 9860942
 REMARK X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 154-270.
 REFERENCE 4 (residues 1 to 505)
 AUTHORS Gong,W., Hao,B. and Chan,M.K.
 TITLE New mechanistic insights from structural studies of the
 oxygen-sensing domain of Bradyrhizobium japonicum FixL
 JOURNAL Biochemistry 39 (14), 3955-3962 (2000)
 MEDLINE 20213243
 PUBMED 10747783
 REMARK X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 154-270.
 COMMENT

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 collaboration between the Swiss Institute of Bioinformatics and
 the EMBL outstation - the European Bioinformatics Institute.
 The original entry is available from <http://www.expasy.ch/sprot>
 and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE OXYGEN SENSOR; MODULATES THE ACTIVITY OF FIXJ,
 A TRANSCRIPTIONAL ACTIVATOR OF NITROGEN FIXATION FIXK GENE. FIXL
 PROBABLY ACTS AS A KINASE THAT PHOSPHORYLATES FIXJ.
 [ENZYME REGULATION] HEMOPROTEIN. THE HEME MOIETY REGULATES THE
 KINASE ACTIVITY.
 [SUBCELLULAR LOCATION] Integral membrane protein. Inner membrane.
 [SIMILARITY] Contains 1 histidine kinase domain.
 [SIMILARITY] Contains 2 PAS (PER-ARNT-SIM) dimerization domains.
 [SIMILARITY] Contains 2 PAS-associated C-terminal (PAC) domains.

FEATURES	Location/Qualifiers
source	1..505 /organism="Bradyrhizobium japonicum" /db_xref="taxon:375"
gene	1..505 /gene="FIXL" /note="synonym: BLL2760"
Protein	1..505 /gene="FIXL" /product="Sensor protein fixL" /EC_number="2.7.3.-"
Region	14..85 /gene="FIXL" /region_name="Domain" /note="PAS 1."
Region	88..140 /gene="FIXL" /region_name="Domain" /note="PAC 1."
Region	141..208 /gene="FIXL" /region_name="Domain" /note="PAS 2."
Region	155..160 /gene="FIXL"

Region /region_name="Beta-strand region"
161..162 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
164..168 /gene="FIXL"
Region /region_name="Beta-strand region"
170..176 /gene="FIXL"
Region /region_name="Helical region"
180..183 /gene="FIXL"
Region /region_name="Helical region"
184..185 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
187 /gene="FIXL"
Region /region_name="Beta-strand region"
188..191 /gene="FIXL"
Region /region_name="Helical region"
194..195 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
196..210 /gene="FIXL"
Site /region_name="Helical region"
200 /gene="FIXL"
Region /site_type="metal-binding"
209..268 /note="IRON (HEME AXIAL LIGAND)."
Region /gene="FIXL"
/region_name="Domain"
/note="PAC 2."
Region 216..218 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
220..225 /gene="FIXL"
Region /region_name="Beta-strand region"
227..228 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
231..243 /gene="FIXL"
Region /region_name="Beta-strand region"
244..245 /gene="FIXL"
Region /region_name="Hydrogen bonded turn"
246..255 /gene="FIXL"
Region /region_name="Beta-strand region"
257..268 /gene="FIXL"
Region /region_name="Helical region"
269 /gene="FIXL"
/region_name="Hydrogen bonded turn"

Region 288..503
/gene="FIXL"
/region_name="Domain"
/note="HISTIDINE KINASE."
Site 291
/gene="FIXL"
/site_type="phosphorylation"
/note="(AUTO-) (BY SIMILARITY)."

ORIGIN

1 maptrvthpp ddgrgehfrv rieggvgtw dldiktwald wsdtartllg igqdqpasyd
61 lflsrlepdd rervesaikr vserggfdfv sfrvagtsna gqwiraragl irdeagtahr
121 lsgifldide ekqvegalrt rethlrsilh tipdamivid ghgiiqlfst aaerlfgwse
181 leaigqnvni lmpepdrrsh dsyisrytt sdphiigigr ivtgkrrdgt tfpmhlsige
241 mqsggepyft gfvrndltehq qtqarlgelq selvhvssrls amgemasala helngplai
301 snymkgsrll lagssdpnpt kvesaldraa equalragqii rrlrdfvarg esekrvesl
361 kliieeagalg lagareqnvq lrfslidpgad lvladrvqiq qvlvnlfrrna leamagsqrr
421 elvvvtntpaa ddmievsvsd tgsgfqddvi pnlfqtffft kdtgmvgvglis isrsiieahg
481 grmwaesnas ggatfrftlp aaden

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Jul 30 2003 12:44:50